

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: OSTERHOFF, CAROLINE
IVELL, RICHARD
- (ii) TITLE OF INVENTION: EPIDIDYMIS-SPECIFIC RECEPTOR PROTEIN
- (iii) NUMBER OF SEQUENCES: 11
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: NIXON & VANDERHYE P.C.
 - (B) STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
 - (C) CITY: ARLINGTON
 - (D) STATE: VA
 - (E) COUNTRY: USA
 - (F) ZIP: 22201
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: SADOFF, B.J.
 - (B) REGISTRATION NUMBER: 36,663
 - (C) REFERENCE/DOCKET NUMBER: 35-125
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 703-816-4000
 - (B) TELEFAX: 703-816-4100

(2) INFORMATION FOR SEQ ID NO: 1:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4665 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..3114

(ix) FEATURE:
 (A) NAME/KEY: 3'UTR
 (B) LOCATION: 3115..4665

(ix) FEATURE:
 (A) NAME/KEY: polyA-site
 (B) LOCATION: 4647..4652
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| AGC CAG CCC GAG GAC GCG AGC GGC AGG TGT GCA CAG AGG TTC TCC ACT | 48  |
| Ser Gln Pro Glu Asp Ala Ser Gly Arg Cys Ala Gln Arg Phe Ser Thr |     |
| 1 5 10 15                                                       |     |
| TTG TTT TCT GAA CTC GCG GTC AGG ATG GTT TTC TCT GTC AGG CAG TGT | 96  |
| Leu Phe Ser Glu Leu Ala Val Arg Met Val Phe Ser Val Arg Gln Cys |     |
| 20 25 30                                                        |     |
| GGC CAT GTT GGC AGA ACT GAA GAA GTT TTA CTG ACG TTC AAG ATA TTC | 144 |
| Gly His Val Gly Arg Thr Glu Glu Val Leu Leu Thr Phe Lys Ile Phe |     |
| 35 40 45                                                        |     |
| CTT GTC ATC ATT TGT CTT CAT GTC GTT CTG GTA ACA TCC CTG GAA GAA | 192 |
| Leu Val Ile Ile Cys Leu His Val Val Leu Val Thr Ser Leu Glu Glu |     |
| 50 55 60                                                        |     |
| GAT ACT GAT AAT TCC AGT TTG TCA CCA CCA CCT GCT AAA TTA TCT GTT | 240 |
| Asp Thr Asp Asn Ser Ser Leu Ser Pro Pro Pro Ala Lys Leu Ser Val |     |
| 65 70 75 80                                                     |     |
| GTC AGT TTT GCC CCC TCC TCC AAT GAG GTT GAA ACA ACA AGC CTC AAT | 288 |
| Val Ser Phe Ala Pro Ser Ser Asn Glu Val Glu Thr Thr Ser Leu Asn |     |
| 85 90 95                                                        |     |
| GAT GTT ACT TTA AGC TTA CTC CCT TCA AAC GAA ACA GAA AAA ACT AAA | 336 |
| Asp Val Thr Leu Ser Leu Leu Pro Ser Asn Glu Thr Glu Lys Thr Lys |     |
| 100 105 110                                                     |     |
| ATC ACT ATA GTA AAA ACC TTC AAT GCT TCA GGC GTC AAA CCC CAG AGA | 384 |
| Ile Thr Ile Val Lys Thr Phe Asn Ala Ser Gly Val Lys Pro Gln Arg |     |
| 115 120 125                                                     |     |
| AAT ATC TGC AAT TTG TCA TCT ATT TGC AAT GAC TCA GCA TTT TTT AGA | 432 |
| Asn Ile Cys Asn Leu Ser Ser Ile Cys Asn Asp Ser Ala Phe Phe Arg |     |
| 130 135 140                                                     |     |
| GGT GAG ATC ATG TTT CAA TAT GAT AAA GAA AGC ACT GTT CCC CAG AAT | 480 |
| Gly Glu Ile Met Phe Gln Tyr Asp Lys Glu Ser Thr Val Pro Gln Asn |     |
| 145 150 155 160                                                 |     |
| CAA CAT ATA ACG AAT GGC ACC TTA ACT GGA GTC CTG TCT CTA AGT GAA | 528 |
| Gln His Ile Thr Asn Gly Thr Leu Thr Gly Val Leu Ser Leu Ser Glu |     |
| 165 170 175                                                     |     |
| TTA AAA CGC TCA GAG CTC AAC AAA ACC CTG CAA ACC CTA AGT GAG ACT | 576 |
| Leu Lys Arg Ser Glu Leu Asn Lys Thr Leu Gln Thr Leu Ser Glu Thr |     |
| 180 185 190                                                     |     |
| TAC TTT ATA ATG TGT GCT ACA GCA GAG GCC CAA AGC ACA TTA AAT TGT | 624 |
| Tyr Phe Ile Met Cys Ala Thr Ala Glu Ala Gln Ser Thr Leu Asn Cys |     |
| 195 200 205                                                     |     |
| ACA TTC ACA ATA AAA CTG AAT AAT ACA ATG AAT GCA TGT GCT GCA ATA | 672 |
| Thr Phe Thr Ile Lys Leu Asn Asn Thr Met Asn Ala Cys Ala Ala Ile |     |
| 210 215 220                                                     |     |
| GCC GCT TTG GAA AGA GTA AAG ATT CGA CCA ATG GAA CAC TGC TGC TGT | 720 |
| Ala Ala Leu Glu Arg Val Lys Ile Arg Pro Met Glu His Cys Cys Cys |     |

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|                                                                                                                                                       |     |     |     |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----|-----|------|
| 225                                                                                                                                                   | 230 | 235 | 240 |      |
| TCT GTC AGG ATA CCC TGC CCT TCC TCC CCA GAA GAG TTG GGA AAG CTT<br>Ser Val Arg Ile Pro Cys Pro Ser Ser Pro Glu Glu Leu Gly Lys Leu<br>245 250 255     |     |     |     | 768  |
| CAG TGT GAC CTG CAG GAT CCC ATT GTC TGT CTT GCT GAC CAT CCA CGT<br>Gln Cys Asp Leu Gln Asp Pro Ile Val Cys Leu Ala Asp His Pro Arg<br>260 265 270     |     |     |     | 816  |
| GGC CCA CCA TTT TCT TCC AGC CAA TCC ATC CCA GTG GTG CCT CGG GCC<br>Gly Pro Pro Phe Ser Ser Ser Gln Ser Ile Pro Val Val Pro Arg Ala<br>275 280 285     |     |     |     | 864  |
| ACT GTG CTT TCC CAG GTC CCC AAA GCT ACC TCT TTT GCT GAG CCT CCA<br>Thr Val Leu Ser Gln Val Pro Lys Ala Thr Ser Phe Ala Glu Pro Pro<br>290 295 300     |     |     |     | 912  |
| GAT TAT TCA CCT GTG ACC CAC AAT GTT CCC TCT CCA ATA GGG GAG ATT<br>Asp Tyr Ser Pro Val Thr His Asn Val Pro Ser Pro Ile Gly Glu Ile<br>305 310 315 320 |     |     |     | 960  |
| CAA CCC CTT TCA CCC CAG CCT TCA GCT CCC ATA GCT TCC AGC CCT GCC<br>Gln Pro Leu Ser Pro Gln Pro Ser Ala Pro Ile Ala Ser Ser Pro Ala<br>325 330 335     |     |     |     | 1008 |
| ATT GAC ATG CCC CCA CAG TCT GAA ACG ATC TCT TCC CCT ATG CCC CAA<br>Ile Asp Met Pro Pro Gln Ser Glu Thr Ile Ser Ser Pro Met Pro Gln<br>340 345 350     |     |     |     | 1056 |
| ACC CAT GTC TCC GGC ACC CCA CCT CCT GTG AAA GCC TCA TTT TCC TCT<br>Thr His Val Ser Gly Thr Pro Pro Pro Val Lys Ala Ser Phe Ser Ser<br>355 360 365     |     |     |     | 1104 |
| CCC ACC GTG TCT GCC CCT GCG AAT GTC AAC ACT ACC AGC GCA CCT CCT<br>Pro Thr Val Ser Ala Pro Ala Asn Val Asn Thr Thr Ser Ala Pro Pro<br>370 375 380     |     |     |     | 1152 |
| GTC CAG ACA GAC ATC GTC AAC ACC AGC AGT ATT TCT GAT CTT GAG AAC<br>Val Gln Thr Asp Ile Val Asn Thr Ser Ser Ile Ser Asp Leu Glu Asn<br>385 390 395 400 |     |     |     | 1200 |
| CAA GTG TTG CAG ATG GAG AAG GCT CTG TCC TTG GGC AGC CTG GAG CCT<br>Gln Val Leu Gln Met Glu Lys Ala Leu Ser Leu Gly Ser Leu Glu Pro<br>405 410 415     |     |     |     | 1248 |
| AAC CTC GCA GGA GAA ATG ATC AAC CAA GTC AGC AGA CTC CTT CAT TCC<br>Asn Leu Ala Gly Glu Met Ile Asn Gln Val Ser Arg Leu Leu His Ser<br>420 425 430     |     |     |     | 1296 |
| CCG CCT GAC ATG CTG GCC CCT CTG GCT CAA AGA TTG CTG AAA GTA GTG<br>Pro Pro Asp Met Leu Ala Pro Leu Ala Gln Arg Leu Leu Lys Val Val<br>435 440 445     |     |     |     | 1344 |
| GAT GAC ATT GGC CTA CAG CTG AAC TTT TCA AAC ACG ACT ATA AGT CTA<br>Asp Asp Ile Gly Leu Gln Leu Asn Phe Ser Asn Thr Thr Ile Ser Leu<br>450 455 460     |     |     |     | 1392 |
| ACC TCC CCT TCT TTG GCT CTG GCT GTG ATC AGA GTG AAT GCC AGT AGT<br>Thr Ser Pro Ser Leu Ala Leu Ala Val Ile Arg Val Asn Ala Ser Ser<br>465 470 475 480 |     |     |     | 1440 |

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|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| TTC AAC ACA ACT ACC TTT GTG GCC CAA GAC CCT GCA AAT CTT CAG GTT<br>Phe Asn Thr Thr Thr Phe Val Ala Gln Asp Pro Ala Asn Leu Gln Val<br>485 490 495     | 1488 |
| TCT CTG GAA ACC CAA GCT CCT GAG AAC AGT ATT GGC ACA ATT ACT CTT<br>Ser Leu Glu Thr Gln Ala Pro Glu Asn Ser Ile Gly Thr Ile Thr Leu<br>500 505 510     | 1536 |
| CCT TCA TCG CTG ATG AAT AAT TTA CCA GCT CAT GAC ATG GAG CTA GCT<br>Pro Ser Ser Leu Met Asn Asn Leu Pro Ala His Asp Met Glu Leu Ala<br>515 520 525     | 1584 |
| TCC AGG GTT CAG TTC AAT TTT TTT GAA ACA CCT GCT TTG TTT CAG GAT<br>Ser Arg Val Gln Phe Asn Phe Phe Glu Thr Pro Ala Leu Phe Gln Asp<br>530 535 540     | 1632 |
| CCT TCC CTG GAG AAC CTC TCT CTG ATC AGC TAC GTC ATA TCA TCG AGT<br>Pro Ser Leu Glu Asn Leu Ser Leu Ile Ser Tyr Val Ile Ser Ser Ser<br>545 550 555 560 | 1680 |
| GTT GCA AAC CTG ACC GTC AGG AAC TTG ACA AGA AAC GTG ACA GTC ACA<br>Val Ala Asn Leu Thr Val Arg Asn Leu Thr Arg Asn Val Thr Val Thr<br>565 570 575     | 1728 |
| TTA AAG CAC ATC AAC CCG AGC CAG GAT GAG TTA ACA GTG AGA TGT GTA<br>Leu Lys His Ile Asn Pro Ser Gln Asp Glu Leu Thr Val Arg Cys Val<br>580 585 590     | 1776 |
| TTT TGG GAC TTG GGC AGA AAT GGT GGC AGA GGA GGC TGG TCA GAC AAT<br>Phe Trp Asp Leu Gly Arg Asn Gly Gly Arg Gly Gly Trp Ser Asp Asn<br>595 600 605     | 1824 |
| GGC TGC TCT GTC AAA GAC AGG AGA TTG AAT GAA ACC ATC TGT ACC TGT<br>Gly Cys Ser Val Lys Asp Arg Arg Leu Asn Glu Thr Ile Cys Thr Cys<br>610 615 620     | 1872 |
| AGC CAT CTA ACA AGC TTC GGC GTT CTG CTG GAC CTA TCT AGG ACA TCT<br>Ser His Leu Thr Ser Phe Gly Val Leu Leu Asp Leu Ser Arg Thr Ser<br>625 630 635 640 | 1920 |
| GTG CTG CCT GCT CAA ATG ATG GCT CTG ACG TTC ATT ACA TAT ATT GGT<br>Val Leu Pro Ala Gln Met Met Ala Leu Thr Phe Ile Thr Tyr Ile Gly<br>645 650 655     | 1968 |
| TGT GGG CTT TCA TCA ATT TTT CTG TCA GTG ACT CTT GTA ACC TAC ATA<br>Cys Gly Leu Ser Ser Ile Phe Leu Ser Val Thr Leu Val Thr Tyr Ile<br>660 665 670     | 2016 |
| GCT TTT GAA AAG ATC CGG AGG GAT TAC CCT TCC AAA ATC CTC ATC CAG<br>Ala Phe Glu Lys Ile Arg Arg Asp Tyr Pro Ser Lys Ile Leu Ile Gln<br>675 680 685     | 2064 |
| CTG TGT GCT GCT CTG CTT CTG CTG AAC CTG GTC TTC CTC CTG GAC TCG<br>Leu Cys Ala Ala Leu Leu Leu Leu Asn Leu Val Phe Leu Leu Asp Ser<br>690 695 700     | 2112 |
| TGG ATT GCT CTG TAT AAG ATG CAA GGC CTC TGC ATC TCA GTG GCT GTA<br>Trp Ile Ala Leu Tyr Lys Met Gln Gly Leu Cys Ile Ser Val Ala Val<br>705 710 715 720 | 2160 |
| TTT CTT CAT TAT TTT CTC TTG GTC TCA TTC ACA TGG ATG GGC CTA GAA<br>Phe Leu His Tyr Phe Leu Leu Val Ser Phe Thr Trp Met Gly Leu Glu                    | 2208 |

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|                                                                                                                                                       |     |     |     |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----|-----|------|
|                                                                                                                                                       | 725 | 730 | 735 |      |
| GCA TTC CAT ATG TAC CTG GCC CTT GTC AAA GTA TTT AAT ACT TAC ATC<br>Ala Phe His Met Tyr Leu Ala Leu Val Lys Val Phe Asn Thr Tyr Ile<br>740 745 750     |     |     |     | 2256 |
| CGA AAA TAC ATC CTT AAA TTC TGC ATT GTC GGT TGG GGG GTA CCA GCT<br>Arg Lys Tyr Ile Leu Lys Phe Cys Ile Val Gly Trp Gly Val Pro Ala<br>755 760 765     |     |     |     | 2304 |
| GTG GTT GTG ACC ATC ATC CTG ACT ATA TCC CCA GAT AAC TAT GGG CTT<br>Val Val Val Thr Ile Ile Leu Thr Ile Ser Pro Asp Asn Tyr Gly Leu<br>770 775 780     |     |     |     | 2352 |
| GGA TCC TAT GGG AAA TTC CCC AAT GGT TCA CCG GAT GAC TTC TGC TGG<br>Gly Ser Tyr Gly Lys Phe Pro Asn Gly Ser Pro Asp Asp Phe Cys Trp<br>785 790 795 800 |     |     |     | 2400 |
| ATC AAC AAC AAT GCA GTA TTC TAC ATT ACG GTG GTG GGA TAT TTC TGT<br>Ile Asn Asn Asn Ala Val Phe Tyr Ile Thr Val Val Gly Tyr Phe Cys<br>805 810 815     |     |     |     | 2448 |
| GTG ATA TTT TTG CTG AAC GTC AGC ATG TTC ATT GTG GTC CTG GTT CAG<br>Val Ile Phe Leu Leu Asn Val Ser Met Phe Ile Val Val Leu Val Gln<br>820 825 830     |     |     |     | 2496 |
| CTC TGT CGA ATT AAA AAG AAG AAG CAA CTG GGA GCC CAG CGA AAA ACC<br>Leu Cys Arg Ile Lys Lys Lys Lys Gln Leu Gly Ala Gln Arg Lys Thr<br>835 840 845     |     |     |     | 2544 |
| AGT ATT CAA GAC CTC AGG AGT ATC GCT GGC CTT ACA TTT TTA CTG GGA<br>Ser Ile Gln Asp Leu Arg Ser Ile Ala Gly Leu Thr Phe Leu Leu Gly<br>850 855 860     |     |     |     | 2592 |
| ATA ACT TGG GGC TTT GCC TTC TTT GCC TGG GGA CCA GTT AAC GTG ACC<br>Ile Thr Trp Gly Phe Ala Phe Phe Ala Trp Gly Pro Val Asn Val Thr<br>865 870 875 880 |     |     |     | 2640 |
| TTC ATG TAT CTG TTT GCC ATC TTT AAT ACC TTA CAA GGA TTT TTC ATA<br>Phe Met Tyr Leu Phe Ala Ile Phe Asn Thr Leu Gln Gly Phe Phe Ile<br>885 890 895     |     |     |     | 2688 |
| TTC ATC TTT TAC TGT GTG GCC AAA GAA AAT GTC AGG AAG CAA TGG AGG<br>Phe Ile Phe Tyr Cys Val Ala Lys Glu Asn Val Arg Lys Gln Trp Arg<br>900 905 910     |     |     |     | 2736 |
| CGG TAT CTT TGT TGT GGA AAG TTA CGG CTG GCT GAA AAT TCT GAC TGG<br>Arg Tyr Leu Cys Cys Gly Lys Leu Arg Leu Ala Glu Asn Ser Asp Trp<br>915 920 925     |     |     |     | 2784 |
| AGT AAA ACT GCT ACT AAT GGT TTA AAG AAG CAG ACT GTA AAC CAA GGA<br>Ser Lys Thr Ala Thr Asn Gly Leu Lys Lys Gln Thr Val Asn Gln Gly<br>930 935 940     |     |     |     | 2832 |
| GTG TCC AGC TCT TCA AAT TCC TTA CAG TCA AGC AGT AAC TCC ACT AAC<br>Val Ser Ser Ser Ser Asn Ser Leu Gln Ser Ser Ser Asn Ser Thr Asn<br>945 950 955 960 |     |     |     | 2880 |
| TCC ACC ACA CTG CTA GTG AAT AAT GAT TGC TCA GTA CAC GCA AGC GGG<br>Ser Thr Thr Leu Leu Val Asn Asn Asp Cys Ser Val His Ala Ser Gly<br>965 970 975     |     |     |     | 2928 |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| AAT GGA AAT GCT TCT ACA GAG AGG AAT GGG GTC TCT TTT AGT GTT CAG   | 2976 |
| Asn Gly Asn Ala Ser Thr Glu Arg Asn Gly Val Ser Phe Ser Val Gln   |      |
| 980 985 990                                                       |      |
| AAT GGA GAT GTG TGC CTT CAC GAT TTC ACT GGA AAA CAG CAC ATG TTT   | 3024 |
| Asn Gly Asp Val Cys Leu His Asp Phe Thr Gly Lys Gln His Met Phe   |      |
| 995 1000 1005                                                     |      |
| AAC GAG AAG GAA GAT TCC TGC AAT GGG AAA GGC CGT ATG GCT CTC AGA   | 3072 |
| Asn Glu Lys Glu Asp Ser Cys Asn Gly Lys Gly Arg Met Ala Leu Arg   |      |
| 1010 1015 1020                                                    |      |
| AGG ACT TCA AAG CGG GGA AGC TTA CAC TTT ATT GAG CAA ATG           | 3114 |
| Arg Thr Ser Lys Arg Gly Ser Leu His Phe Ile Glu Gln Met           |      |
| 1025 1030 1035                                                    |      |
| TGATTCCCTTT CTTCTAAAT CAAAGCATGA TGCTTGACAG TGTGAAATGT CCAATTTTAC | 3174 |
| CTTTTACACA ATGTGAGATG TATGAAAATC AACTCATTTT ATTCTCGGCA ACATCTGGAG | 3234 |
| AAGCATAAGC TAATTAAGGG CGATGATTAT TATTACAAGA AGAAACCAAG ACATTACACC | 3294 |
| ATGGTTTTTA GACATTTCTG ATTTGGTTTC TTATCTTTCA TTTTATAAGA AGGTTGGTTT | 3354 |
| TAAACAATAC ACTAAGAATG ACTCCTATAA AGAAAACAAA AAAAGGTAGT GAACTTTCAG | 3414 |
| CTACCTTTTA AAGAGGCTAA GTTATCTTTG ATAACATCAT ATAAAGCAAC TGTTGACTTC | 3474 |
| AGCCTGTTGG TGAGTTTAGT TGTGCATGCC TTTGTTGTAT ATAAGCTAAA TTCTAGTGAC | 3534 |
| CCATGTGTCA AAAATCTTAC TTCTACATTT TTTTGTATTT ATTTTCTACT GTGTAAATGT | 3594 |
| ATTCCTTTGT AGAATCATGG TTGTTTTGTC TCACGTGATA ATTCAGAAAA TCCTTGCTCG | 3654 |
| TTCCGCAAAT CCTAAAGCTC CTTTTGGAGA TGATATAGGA TGTGAAATAC AGAAACCTCA | 3714 |
| GTGAAATCAA GAAATAATGA TCCCAGCCAG ACTGAGAAAA TGTAAGCAGA CAGTGCCACA | 3774 |
| GTTAGCTCAT ACAGTGCCTT TGAGCAAGTT AGGAAAAGAT GCCCCCACTG GGCAGACACA | 3834 |
| GCCCTATGGG TCATGGTTTG ACAAACAGAG TGAGAGACCA TATTTTAGCC CCACTCACCC | 3894 |
| TCTTNGGTGC ACGACCTGTA CAGCCAAACA CAGCATCCAA TATGAATACC CATCCCCTGA | 3954 |
| CCGCATCCCC AGTAGTCAGA TTATAGAATC TGCACCAAGA TGTTTAGCTT TATACCTTGG | 4014 |
| CCACAGAGAG GGATGAACTG TCATCCAGAC CATGTGTCAG GAAAATTGTG AACGTAGATG | 4074 |
| AGGTACATAC ACTGCCGCTT CTCAAATCCC CAGAGCCTTT AGGAACAGGA GAGTAGACTA | 4134 |
| GGATTCTTTC TCTTAAAAAG GTACATATAT ATGGAAAAAA ATCATATTGC CGTTCTTTAA | 4194 |
| AAGGCAACTG CATGGTACAT TGTTGATTGT TATGACTGGT ACACTCTGGC CCAGCCAGAG | 4254 |
| CTATAATTGT TTTTAAATG TGTCTTGAAG AATGCACAGT GANAAGGGGA GTAGCTATTG  | 4314 |
| GGAACAGGGA ACTGTCCTAC ACTGCTATTG TTGCTACATG TATCGAGCCT TGATTGCTCC | 4374 |
| TAGTTATATA CAGGGTCTAT CTTGCTTCCT ACCTACATCT GCTTGAGCAG TGCCTCAAGT | 4434 |
| ACATCCTTAT TAGGAACATT TCAAACCCCT TTTAGTTAAG TCTTTCATA AGTTCTCTT   | 4494 |

GCATATATTT CAAGTGAATG TTGGATCTCA GACTAACCAT AGTAATAATA CACATTTCTG 4554  
 TGAGTGCTGA CTTGTCTTTG CAATATTTCT TTTCTGATTT ATTTAATTTT CTTGTATTTA 4614  
 TATGTTAAAA TCAAAAATGT TAAAATCAAT GAAATAAATT TGCAGTTAAG A 4665

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1038 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Ser Gln Pro Glu Asp Ala Ser Gly Arg Cys Ala Gln Arg Phe Ser Thr  
 1 5 10 15  
 Leu Phe Ser Glu Leu Ala Val Arg Met Val Phe Ser Val Arg Gln Cys  
 20 25 30  
 Gly His Val Gly Arg Thr Glu Glu Val Leu Leu Thr Phe Lys Ile Phe  
 35 40 45  
 Leu Val Ile Ile Cys Leu His Val Val Leu Val Thr Ser Leu Glu Glu  
 50 55 60  
 Asp Thr Asp Asn Ser Ser Leu Ser Pro Pro Pro Ala Lys Leu Ser Val  
 65 70 75 80  
 Val Ser Phe Ala Pro Ser Ser Asn Glu Val Glu Thr Thr Ser Leu Asn  
 85 90 95  
 Asp Val Thr Leu Ser Leu Leu Pro Ser Asn Glu Thr Glu Lys Thr Lys  
 100 105 110  
 Ile Thr Ile Val Lys Thr Phe Asn Ala Ser Gly Val Lys Pro Gln Arg  
 115 120 125  
 Asn Ile Cys Asn Leu Ser Ser Ile Cys Asn Asp Ser Ala Phe Phe Arg  
 130 135 140  
 Gly Glu Ile Met Phe Gln Tyr Asp Lys Glu Ser Thr Val Pro Gln Asn  
 145 150 155 160  
 Gln His Ile Thr Asn Gly Thr Leu Thr Gly Val Leu Ser Leu Ser Glu  
 165 170 175  
 Leu Lys Arg Ser Glu Leu Asn Lys Thr Leu Gln Thr Leu Ser Glu Thr  
 180 185 190  
 Tyr Phe Ile Met Cys Ala Thr Ala Glu Ala Gln Ser Thr Leu Asn Cys  
 195 200 205  
 Thr Phe Thr Ile Lys Leu Asn Asn Thr Met Asn Ala Cys Ala Ala Ile  
 210 215 220

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Ala Ala Leu Glu Arg Val Lys Ile Arg Pro Met Glu His Cys Cys Cys  
 225 230 235 240

Ser Val Arg Ile Pro Cys Pro Ser Ser Pro Glu Glu Leu Gly Lys Leu  
 245 250 255

Gln Cys Asp Leu Gln Asp Pro Ile Val Cys Leu Ala Asp His Pro Arg  
 260 265 270

Gly Pro Pro Phe Ser Ser Ser Gln Ser Ile Pro Val Val Pro Arg Ala  
 275 280 285

Thr Val Leu Ser Gln Val Pro Lys Ala Thr Ser Phe Ala Glu Pro Pro  
 290 295 300

Asp Tyr Ser Pro Val Thr His Asn Val Pro Ser Pro Ile Gly Glu Ile  
 305 310 315 320

Gln Pro Leu Ser Pro Gln Pro Ser Ala Pro Ile Ala Ser Ser Pro Ala  
 325 330 335

Ile Asp Met Pro Pro Gln Ser Glu Thr Ile Ser Ser Pro Met Pro Gln  
 340 345 350

Thr His Val Ser Gly Thr Pro Pro Pro Val Lys Ala Ser Phe Ser Ser  
 355 360 365

Pro Thr Val Ser Ala Pro Ala Asn Val Asn Thr Thr Ser Ala Pro Pro  
 370 375 380

Val Gln Thr Asp Ile Val Asn Thr Ser Ser Ile Ser Asp Leu Glu Asn  
 385 390 395 400

Gln Val Leu Gln Met Glu Lys Ala Leu Ser Leu Gly Ser Leu Glu Pro  
 405 410 415

Asn Leu Ala Gly Glu Met Ile Asn Gln Val Ser Arg Leu Leu His Ser  
 420 425 430

Pro Pro Asp Met Leu Ala Pro Leu Ala Gln Arg Leu Leu Lys Val Val  
 435 440 445

Asp Asp Ile Gly Leu Gln Leu Asn Phe Ser Asn Thr Thr Ile Ser Leu  
 450 455 460

Thr Ser Pro Ser Leu Ala Leu Ala Val Ile Arg Val Asn Ala Ser Ser  
 465 470 475 480

Phe Asn Thr Thr Thr Phe Val Ala Gln Asp Pro Ala Asn Leu Gln Val  
 485 490 495

Ser Leu Glu Thr Gln Ala Pro Glu Asn Ser Ile Gly Thr Ile Thr Leu  
 500 505 510

Pro Ser Ser Leu Met Asn Asn Leu Pro Ala His Asp Met Glu Leu Ala  
 515 520 525

Ser Arg Val Gln Phe Asn Phe Phe Glu Thr Pro Ala Leu Phe Gln Asp  
 530 535 540

Pro Ser Leu Glu Asn Leu Ser Leu Ile Ser Tyr Val Ile Ser Ser Ser  
 545 550 555 560

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Val Ala Asn Leu Thr Val Arg Asn Leu Thr Arg Asn Val Thr Val Thr  
565 570 575

Leu Lys His Ile Asn Pro Ser Gln Asp Glu Leu Thr Val Arg Cys Val  
580 585 590

Phe Trp Asp Leu Gly Arg Asn Gly Gly Arg Gly Gly Trp Ser Asp Asn  
595 600 605

Gly Cys Ser Val Lys Asp Arg Arg Leu Asn Glu Thr Ile Cys Thr Cys  
610 615 620

Ser His Leu Thr Ser Phe Gly Val Leu Leu Asp Leu Ser Arg Thr Ser  
625 630 635 640

Val Leu Pro Ala Gln Met Met Ala Leu Thr Phe Ile Thr Tyr Ile Gly  
645 650 655

Cys Gly Leu Ser Ser Ile Phe Leu Ser Val Thr Leu Val Thr Tyr Ile  
660 665 670

Ala Phe Glu Lys Ile Arg Arg Asp Tyr Pro Ser Lys Ile Leu Ile Gln  
675 680 685

Leu Cys Ala Ala Leu Leu Leu Leu Asn Leu Val Phe Leu Leu Asp Ser  
690 695 700

Trp Ile Ala Leu Tyr Lys Met Gln Gly Leu Cys Ile Ser Val Ala Val  
705 710 715 720

Phe Leu His Tyr Phe Leu Leu Val Ser Phe Thr Trp Met Gly Leu Glu  
725 730 735

Ala Phe His Met Tyr Leu Ala Leu Val Lys Val Phe Asn Thr Tyr Ile  
740 745 750

Arg Lys Tyr Ile Leu Lys Phe Cys Ile Val Gly Trp Gly Val Pro Ala  
755 760 765

Val Val Val Thr Ile Ile Leu Thr Ile Ser Pro Asp Asn Tyr Gly Leu  
770 775 780

Gly Ser Tyr Gly Lys Phe Pro Asn Gly Ser Pro Asp Asp Phe Cys Trp  
785 790 795 800

Ile Asn Asn Asn Ala Val Phe Tyr Ile Thr Val Val Gly Tyr Phe Cys  
805 810 815

Val Ile Phe Leu Leu Asn Val Ser Met Phe Ile Val Val Leu Val Gln  
820 825 830

Leu Cys Arg Ile Lys Lys Lys Lys Gln Leu Gly Ala Gln Arg Lys Thr  
835 840 845

Ser Ile Gln Asp Leu Arg Ser Ile Ala Gly Leu Thr Phe Leu Leu Gly  
850 855 860

Ile Thr Trp Gly Phe Ala Phe Phe Ala Trp Gly Pro Val Asn Val Thr  
865 870 875 880

Phe Met Tyr Leu Phe Ala Ile Phe Asn Thr Leu Gln Gly Phe Phe Ile

|                                                                 |      |      |
|-----------------------------------------------------------------|------|------|
| 885                                                             | 890  | 895  |
| Phe Ile Phe Tyr Cys Val Ala Lys Glu Asn Val Arg Lys Gln Trp Arg |      |      |
| 900                                                             | 905  | 910  |
| Arg Tyr Leu Cys Cys Gly Lys Leu Arg Leu Ala Glu Asn Ser Asp Trp |      |      |
| 915                                                             | 920  | 925  |
| Ser Lys Thr Ala Thr Asn Gly Leu Lys Lys Gln Thr Val Asn Gln Gly |      |      |
| 930                                                             | 935  | 940  |
| Val Ser Ser Ser Ser Asn Ser Leu Gln Ser Ser Ser Asn Ser Thr Asn |      |      |
| 945                                                             | 950  | 955  |
| Ser Thr Thr Leu Leu Val Asn Asn Asp Cys Ser Val His Ala Ser Gly |      |      |
| 965                                                             | 970  | 975  |
| Asn Gly Asn Ala Ser Thr Glu Arg Asn Gly Val Ser Phe Ser Val Gln |      |      |
| 980                                                             | 985  | 990  |
| Asn Gly Asp Val Cys Leu His Asp Phe Thr Gly Lys Gln His Met Phe |      |      |
| 995                                                             | 1000 | 1005 |
| Asn Glu Lys Glu Asp Ser Cys Asn Gly Lys Gly Arg Met Ala Leu Arg |      |      |
| 1010                                                            | 1015 | 1020 |
| Arg Thr Ser Lys Arg Gly Ser Leu His Phe Ile Glu Gln Met         |      |      |
| 1025                                                            | 1030 | 1035 |

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Phe | Phe | Arg | Gly | Glu | Ile | Met | Phe | Gln | Tyr | Asp | Lys | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

0073457-120800

Cys Leu Ala Asp His Pro Arg Gly Pro Pro Phe Ser Ser Ser Gln  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Gly Ser Tyr Gly Lys Phe Pro Asn Gly Ser Pro Asp Asp Phe Cys  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 6:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Cys Trp Ile Asn Asn Asn Ala Val Phe Tyr  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Cys Arg Ile Lys Lys Lys Lys Gln Leu Gly Ala Gln Arg Lys Thr  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:

00731657-120800

(ii) MOLECULE TYPE: cDNA

AGCTATGGGA GCTGAAG

17

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

TGTCAATGGC AGGGCTG

17

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

CATCCGAAAA TACATCC

17

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

TGAAGGCACA CATCTCC

17